

OIPF

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/788,626

DATE: 06/26/2001

TIME: 07:31:46

Input Set : A:\401.app.txt

Output Set: N:\CRF3\06262001\I788626.raw

ENTERED

```

4 <110> APPLICANT: Flint, Andrew J.
5      Cbol, Deborah E.
8 <120> TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
9      PHOSPHATES
11 <130> FILE REFERENCE: 200125.401
13 <140> CURRENT APPLICATION NUMBER: US/09/788,626
14 <141> CURRENT FILING DATE: 2001-02-13
16 <160> NUMBER OF SEQ ID NOS: 40
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 11
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <221> NAME/KEY: VARIANT
27 <222> LOCATION: (1)...(1)
28 <223> OTHER INFORMATION: Xaa = Ile or Val
30 <221> NAME/KEY: VARIANT
31 <222> LOCATION: (4)...(4)
32 <223> OTHER INFORMATION: Xaa = any amino acid
34 <221> NAME/KEY: VARIANT
35 <222> LOCATION: (7)...(7)
36 <223> OTHER INFORMATION: Xaa = any amino acid
38 <221> NAME/KEY: VARIANT
39 <222> LOCATION: (8)...(8)
40 <223> OTHER INFORMATION: Xaa = any amino acid
42 <221> NAME/KEY: VARIANT
43 <222> LOCATION: (10)...(10)
44 <223> OTHER INFORMATION: Xaa = Ser or Thr
46 <223> OTHER INFORMATION: Unique signature sequence motif which is invariant
47      among all PTPs.
49 <400> SEQUENCE: 1
W--> 50 Xaa His Cys Xaa Ala Gly Xaa Xaa Arg Xaa Gly
51      1          5          10
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 254
55 <212> TYPE: PRT
56 <213> ORGANISM: Homo sapiens
58 <400> SEQUENCE: 2
59 Asp Phe Pro Cys Arg Val Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn
60      1          5          10          15
61 Arg Tyr Arg Asp Val Ser Pro Phe Asp His Ser Arg Ile Lys Leu His
62      20          25          30
63 Gln Glu Asp Asn Asp Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu
64      35          40          45
65 Ala Gln Arg Ser Tyr Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys
66      50          55          60

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67 Gly His Phe Trp Glu Met Val Trp Glu Gln Lys Ser Arg Gly Val Val
68 65 70 75 80
69 Met Leu Asn Arg Val Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr
70 85 90 95
71 Trp Pro Gln Lys Glu Glu Lys Glu Met Ile Phe Glu Asp Thr Asn Leu
72 100 105 110
73 Lys Leu Thr Leu Ile Ser Glu Asp Ile Lys Ser Tyr Tyr Thr Val Leu
74 115 120 125
75 Glu Leu Glu Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe
76 130 135 140
77 His Tyr Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser
78 145 150 155 160
79 Phe Leu Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro
80 165 170 175
81 Glu His Gly Pro Val Val Val His Cys Ser Ala Gly Ile Gly Arg Ser
82 180 185 190
83 Gly Thr Phe Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg
84 195 200 205
85 Lys Asp Pro Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg
86 210 215 220
87 Lys Phe Arg Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser
88 225 230 235 240
89 Tyr Leu Ala Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp
90 245 250
92 <210> SEQ ID NO: 3
93 <211> LENGTH: 251
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 3
98 Asp Tyr Pro His Arg Val Ala Lys Phe Pro Glu Asn Arg Asn Arg Asn
99 1 5 10 15
100 Arg Tyr Arg Asp Val Ser Pro Tyr Asp His Ser Arg Val Leu Gln Asn
101 20 25 30
102 Ala Glu Asn Asp Tyr Ile Asn Ala Ser Leu Val Asp Ile Glu Glu Ala
103 35 40 45
104 Gln Arg Ser Tyr Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Cys
105 50 55 60
106 His Phe Trp Leu Met Val Trp Gln Gln Lys Thr Lys Ala Val Val Met
107 65 70 75 80
108 Leu Asn Arg Ile Val Glu Lys Glu Ser Val Lys Cys Ala Gln Tyr Trp
109 85 90 95
110 Pro Thr Asp Asp Gln Glu Met Leu Phe Lys Glu Thr Gly Phe Ser Val
111 100 105 110
112 Lys Leu Leu Ser Glu Asp Val Lys Ser Tyr Tyr Thr Val Leu Gln Leu
113 115 120 125
114 Glu Asn Ile Asn Ser Gly Glu Thr Arg Thr Ile Ser His Phe His Tyr
115 130 135 140
116 Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu
117 145 150 155 160

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118 Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Asn Pro Asp His
119                               165                170                175
120 Gly Pro Ala Val Ile His Cys Ser Ala Gly Ile Gly Arg Ser Gly Thr
121                               180                185                190
122 Phe Ser Leu Val Asp Thr Cys Leu Val Leu Met Glu Lys Gly Asp Asp
123                               195                200                205
124 Ile Asn Ile Lys Gln Val Leu Leu Asn Met Arg Lys Tyr Arg Met Gly
125                               210                215                220
126 Leu Ile Gln Thr Pro Asp Gln Leu Arg Phe Ser Tyr Met Ala Ile Ile
127 225                               230                235                240
128 Glu Gly Ala Lys Cys Ile Lys Gly Asp Ser Ser
129                               245                250
131 <210> SEQ ID NO: 4
132 <211> LENGTH: 317
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 4
137 Gly Ile Thr Ala Asp Ser Ser Asn His Pro Asp Asn Lys His Lys Asn
138 1                               5                10                15
139 Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser Arg Val Lys Leu Ala
140                               20                25                30
141 Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp Tyr Ile Asn Ala Asn
142                               35                40                45
143 Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr Ile Ala Ala Gln Gly
144                               50                55                60
145 Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg Met Ile Trp Glu His
146 65                               70                75                80
147 Asn Val Glu Val Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
148                               85                90                95
149 Arg Lys Cys Asp Gln Tyr Trp Pro Pro Ala Asp Gly Ser Glu Glu Tyr
150                               100               105               110
151 Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr Tyr
152                               115               120               125
153 Thr Val Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys Gly Ser Gln Lys
154                               130               135               140
155 Gly Arg Pro Ser Gly Arg Val Val Thr Gln Tyr His Tyr Thr Gln Trp
156 145                               150               155               160
157 Pro Asp Met Gly Val Pro Glu Tyr Ser Leu Pro Val Leu Thr Phe Val
158                               165               170               175
159 Arg Lys Ala Ala Tyr Ala Lys Arg His Ala Val Gly Pro Val Val Val
160                               180               185               190
161 His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Leu Asp
162                               195               200               205
163 Ser Met Leu Gln Gln Ile Gln His Glu Gly Thr Val Asn Ile Phe Gly
164                               210               215               220
165 Phe Leu Lys His Ile Arg Ser Gln Arg Asn Tyr Leu Val Gln Thr Glu
166 225                               230               235               240
167 Glu Gln Tyr Val Phe Ile His Asp Thr Leu Val Glu Ala Ile Leu Ser
168                               245               250               255

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```

169 Lys Glu Thr Glu Val Val Leu Asp Ser Met Leu Gln Gln Ile Gln His
170          260          265          270
171 Glu Gly Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln
172          275          280          285
173 Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp
174          290          295          300
175 Thr Leu Val Glu Ala Ile Leu Ser Lys Glu Thr Glu Val
176 305          310          315
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 316
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 5
184 Gly Ile Thr Ala Asp Ser Ser Asn His Pro Asp Asn Lys His Lys Asn
185 1          5          10          15
186 Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser Arg Val Lys Leu Ala
187          20          25          30
188 Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp Tyr Ile Asn Ala Asn
189          35          40          45
190 Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr Ile Ala Ala Gln Gly
191          50          55          60
192 Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg Met Ile Trp Glu His
193 65          70          75          80
194 Asn Val Glu Val Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
195          85          90          95
196 Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly Ser Glu Glu Tyr Gly
197          100          105          110
198 Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr Tyr Thr
199          115          120          125
200 Val Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys Gly Ser Gln Lys Gly
201          130          135          140
202 Arg Pro Ser Gly Arg Val Val Thr Gln Tyr His Tyr Thr Gln Trp Pro
203 145          150          155          160
204 Asp Met Gly Val Pro Glu Tyr Ser Leu Pro Val Leu Thr Phe Val Arg
205          165          170          175
206 Lys Ala Ala Tyr Ala Lys Arg His Ala Val Gly Pro Val Val Val His
207          180          185          190
208 Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Leu Asp Ser
209          195          200          205
210 Met Leu Gln Gln Ile Gln His Glu Gly Thr Val Asn Ile Phe Gly Phe
211          210          215          220
212 Leu Lys His Ile Arg Ser Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu
213 225          230          235          240
214 Gln Tyr Val Phe Ile His Asp Thr Leu Val Glu Ala Ile Leu Ser Lys
215          245          250          255
216 Glu Thr Glu Val Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu
217          260          265          270
218 Gly Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg
219          275          280          285

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```

220 Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Thr
221      290                      295                      300
222 Leu Val Glu Ala Ile Leu Ser Lys Glu Thr Glu Val
223 305                      310                      315
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 319
227 <212> TYPE: PRI
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 6
231 Asn Ile Thr Ala Glu His Ser Asn His Pro Glu Asn Lys His Lys Asn
232 1                      5                      10                      15
233 Arg Tyr Ile Asn Ile Leu Ala Tyr Asp His Ser Arg Val Lys Leu Arg
234      20                      25                      30
235 Pro Leu Pro Gly Lys Asp Ser Lys His Ser Asp Tyr Ile Asn Ala Asn
236      35                      40                      45
237 Tyr Val Asp Gly Tyr Asn Lys Ala Lys Ala Tyr Ile Ala Thr Gln Gly
238      50                      55                      60
239 Pro Leu Lys Ser Thr Phe Glu Asp Phe Trp Arg Met Ile Trp Glu Gln
240 65                      70                      75                      80
241 Asn Thr Gly Ile Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
242      85                      90                      95
243 Arg Lys Cys Asp Gln Tyr Trp Pro Thr Glu Asn Ser Glu Glu Tyr Gly
244      100                     105                     110
245 Asn Ile Ile Val Thr Leu Lys Ser Thr Lys Ile His Ala Cys Tyr Thr
246      115                     120                     125
247 Val Phe Ser Ile Arg Asn Thr Lys Val Lys Lys Gly Gln Lys Gly Asn
248      130                     135                     140
249 Pro Lys Gly Arg Gln Asn Glu Arg Val Val Ile Gln Tyr His Tyr Thr
250 145                     150                     155                     160
251 Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ala Leu Pro Val Leu Thr
252      165                     170                     175
253 Phe Val Arg Arg Ser Ser Ala Ala Arg Met Pro Glu Thr Gly Pro Val
254      180                     185                     190
255 Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Val
256      195                     200                     205
257 Ile Asp Ser Met Leu Gln Gln Ile Lys Asp Lys Ser Thr Val Asn Val
258      210                     215                     220
259 Leu Gly Phe Leu Lys His Ile Arg Thr Gln Arg Asn Tyr Leu Val Gln
260 225                     230                     235                     240
261 Thr Glu Glu Gln Tyr Ile Phe Ile His Asp Ala Leu Leu Glu Ala Ile
262      245                     250                     255
263 Leu Gly Lys Glu Thr Glu Val Val Ile Asp Ser Met Leu Gln Gln Ile
264      260                     265                     270
265 Lys Asp Lys Ser Thr Val Asn Val Leu Gly Phe Leu Lys His Ile Arg
266      275                     280                     285
267 Thr Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Ile Phe Ile
268      290                     295                     300
269 His Asp Ala Leu Leu Glu Ala Ile Leu Gly Lys Glu Thr Glu Val
270 305                     310                     315

```

VERIFICATION SUMMARY

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Input Set : A:\401.app.txt

Output Set: N:\CRF3\06262001\I788626.raw

L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1